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Sequence Listing was accepted.
See attached Validation Report.
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Reviewer: Durreshwar Anjum
Timestamp: [year=2009; month=1; day=8; hr=9; min=24; sec=14; ms=912;]
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Validated By CRFValidator v 1.0.3

Application No: 10547532 Version No: 3.0

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Finished: 2009-01-06 15:23:05.946
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Total Errors: 2
No. of SeqIDs Defined: 21
Actual SeqID Count: 21

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<120> MEDICINAL USE OF MIP-3a INHIBITOR AND METHOD OF SCREENING BRAIN/NERVE CELL PROTECTIVE AGENT

<130> 20039.0001USWO

<140> 10547532
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<150> PCT/JP2004/002774
<151> 2004-03-04

<150> JP 2003-056885
<151> 2003-03-04

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Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys
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tgt ctt gga tac aca gac cgt att ctt cat cct aaa ttt att gtg ggc      144
Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
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ttc aca cgg cag ctg gcc aat gaa ggc tgt gac atc aat gct atc atc      192
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    40                  45                  50
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Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
        25                  30                  35
Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
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gct tac ctc tgc agc cag tca gaa gca gca agc aac ttt gac tgc tgc       96
Ala Tyr Leu Cys Ser Gln Ser Glu Ala Ala Ser Asn Phe Asp Cys Cys
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ctc acg tac aca aag aac gtg tat cat cat gcg aga aat ttt gtg ggt      144
Leu Thr Tyr Thr Lys Asn Val Tyr His His Ala Arg Asn Phe Val Gly
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        10                  15                  20
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ttt cac ctg aag tcg aaa aga tcc gtg tgc gct gac cca aag cag atc      240
Phe His Leu Lys Ser Lys Arg Ser Val Cys Ala Asp Pro Lys Gln Ile
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tgg gtg aaa agg att ttg cac ctc ctc agc cta aga acc aag aag atg      288
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Phe His Leu Lys Ser Lys Arg Ser Val Cys Ala Asp Pro Lys Gln Ile
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Leu Leu Ala His Leu Cys Ser Gln Ala Glu Ala Ala Ser Asn Tyr Asp
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ggt ttc aca aga cag atg gcc gat gaa gct tgt gac att aat gct atc      192
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            25                  30                  35
atc ttt cac acg aag aaa aga aaa tct gtg tgc gct gat cca aag cag      240
Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln
        40                  45                  50
aac tgg gtg aaa agg gct gtg aac ctc ctc agc cta aga gtc aag aag      288
Asn Trp Val Lys Arg Ala Val Asn Leu Leu Ser Leu Arg Val Lys Lys
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Met
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Cys Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile Val
                10                  15                  20
Gly Phe Thr Arg Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile
            25                  30                  35
Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln
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Met
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gat tat ttt gtg tca gtc aat act tca tat tac tca gtt gat tct gag       96
Asp Tyr Phe Val Ser Val Asn Thr Ser Tyr Tyr Ser Val Asp Ser Glu
            20                  25                  30
atg tta ctg tgc tcc ttg cag gag gtc agg cag ttc tcc agg cta ttt      144
Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe
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att ctg gtg gtg atc acc ttt gct ttt tat aag aag gcc agg tct atg      240
Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met
65                  70                  75                  80
aca gac gtc tat ctc ttg aac atg gcc att gca gac atc ctc ttt gtt      288
Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val
                85                  90                  95
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Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val
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        115                 120                 125
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Phe Asn Cys Gly Met Leu Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr
    130                 135                 140
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Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr
145                 150                 155                 160
cta ccg cgc agc aaa atc atc tgc ctt gtt gtg tgg ggg ctg tca gtc      528
Leu Pro Arg Ser Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val
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atc atc tcc agc tca act ttt gtc ttc aac caa aaa tac aac acc caa      576
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Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile
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agg tgg aag ctg ctg atg ttg ggg ctt gag cta ctc ttt ggt ttc ttt      672
Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Leu Phe Gly Phe Phe
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ata gct gtg gtg ctt gtg ttt ctg gct tgt cag att cct cat aac atg      816
Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met
            260                 265                 270
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Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys
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cag agc gaa aag cta att ggc tat acg aaa act gtc aca gaa gtc ctg      912
Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu
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gct ttc ctg cac tgc tgc ctg aac cct gtg ctc tac gct ttt att ggg      960
Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly
305                 310                 315                 320
cag aag ttc aga aac tac ttt ctg aag atc ttg aag gac ctg tgg tgt     1008
Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys
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Val Arg Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr
            340                 345                 350
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gcg tcg tcc ttc act atg                                         1122
Ala Ser Ser Phe Thr Met
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            20                  25                  30
Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe
        35                  40                  45
Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn
    50                  55                  60
Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met
65                  70                  75                  80
Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val
                85                  90                  95
Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val
            100                 105                 110
Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn
        115                 120                 125
Phe Asn Cys Gly Met Leu Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr
    130                 135                 140
Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr
145                 150                 155                 160
Leu Pro Arg Ser Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val
                165                 170                 175
Ile Ile Ser Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln
            180                 185                 190
Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile
        195                 200                 205
Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Leu Phe Gly Phe Phe
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Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr
225                 230                 235                 240
Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile
                245                 250                 255
Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met
            260                 265                 270
Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys
        275                 280                 285
Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu
    290                 295                 300
Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly
305                 310                 315                 320
Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys
                325                 330                 335
Val Arg Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr
            340                 345                 350
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Ala Ser Ser Phe Thr Met
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Glu Tyr Tyr Ser Ile Pro Pro Asp His Gly Pro Cys Ser Leu Glu Glu
            20                  25                  30
gtc aga aac ttc acc aag gta ttt gtg cca att gcc tac tcc tta ata      144
Val Arg Asn Phe Thr Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile
        35                  40                  45
tgt gtc ttt ggc ctc ctg ggc aac att atg gtg gtg atg acc ttt gcc      192
Cys Val Phe Gly Leu Leu Gly Asn Ile Met Val Val Met Thr Phe Ala
    50                  55                  60
ttc tac aag aaa gcc aga tcc atg act gac gtc tac ctg ttg aac atg      240
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